

Figure 1A

1	CTGCGACCGGTCTGCCACTGCCAGGTGACCGCTGATGGGAAGACCAGCTGTGTGCAG	60
61	GGAAAGCGAGGTGGGGATGGCGTGCCTGCTACGGACACCTGCTCCACGAGGTGCAGAA	120
121	GGCCACGCAGACAGGCCGGTGTCTGCAGCTGAGGGTCGCCGTGGCCATGATGGACCA	180
1	M M D Q	4
181	GGGCTGCCGGAAATCCTTACCAACAGCGGGCCCTTCACCGTGCTGGTGCCATCCGTCTC	240
5	G C R E I L T T A G P F T V L V P S V S	24
241	CTCCTTCTCCTCCAGGACCATGAATGCATCCCTGCCCAGCAGCTCTGTAGACAGCACAT	300
25	S F S S R T M N A S L A Q Q L C R Q H I	44
301	CATCGCAGGGCAGCACATCCTGGAGGACACAAGGACCCAACAAACACGAAGGTGGTGGAC	360
45	I A G Q H I L E D T R T Q Q T R R W W T	64
361	GCTGGCCGGCAGGAGATCACCGTCACCTTAACCAATTACGAAATACTCCTACAAGTA	420
65	L A G Q E I T V T F N Q F T K Y S Y K Y	84
421	CAAAGACCAGCCCCAGCAGACGTTCAACATCTACAAGGCCAACACATAGCAGCTAATGG	480
85	K D Q P Q Q T F N I Y K A N N I A A N G	104
481	CGTCTTCCACGTGGTCACTGGCCTGGGGCAGGGCCCTCTGGGACCCCTGGGATCC	540
105	V F H V V T G L R W Q A P S G T P G D P	124
541	CAAGAGAACTATCGGACAGATCCTCGCCTCTACCGAGGCCTTCAGCGCTTGAAACCAT	600
125	K R T I G Q I L A S T E A F S R F E T I	144
601	CCTGGAGAACTGTGGGCTGCCCTCCATCCTGGACGGACCTGGGCCCTCACAGTCTTGC	660
145	L E N C G L P S I L D G P G P F T V F A	164
661	CCCAAGCAATGAGGCTGTGGACAGCTTGCCTGACGGCCGCTGATCTACCTCTCACAGC	720
165	P S N E A V D S L R D G R L I Y L F T A	184
721	GGGTCTCTAAACTGCAGGAGTTGGTGGCTACACATCTACAACCACGGCCAGCTGAC	780
185	G L S K L Q E L V R Y H I Y N H G Q L T	204
781	CGTTGAGAAGCTCATCTCCAAGGGTGGATCCTCACCATGGCGAACCGAGTCCTGGCTGT	840
205	V E K L I S K G R I L T M A N Q V L A V	224

Figure 1B

841	GAACATTTCTGAGGAGGGCGCATCTGCTGGACCCGAGGGGGTCCCGCTGCAGAGGGT	900
225	N I S E E G R I L L G P E G V P L Q R V	244
901	AGACGTGATGGCCGCCAATGGCGTGATCCACATGCTGGACGGCATCCCTGCTGCCCGAC	960
245	D V M A A N G V I H M L D G I L L P P T	264
961	CATCCCTGCCCATCCTGCCCAAGCAGTCAGCGAGGGAGCAGCACAAAGATTGTGGCGGGCTC	1020
265	I L P I L P K H C S E E Q H K I V A G S	284
1021	CTGTGTGGACTGCCAAGCCCTGAACACCAGCACCGTGTCCCCAACAGTGTGAAGCTGGA	1080
285	C V D C Q A L N T S T C P P N S V K L D	304
1081	CATCTCCCCAAGGAGTGTGTCTACATCCATGACCCAAACGGGCTCAATGTGCTAAAGAA	1140
305	I F P K E C V Y I H D P T G L N V L K K	324
1141	GGGCTGTGCCAGCTACTGCAACCAAACCATCATGGAACAAGGCTGCTGCAAAGGTTTT	1200
325	G C A S Y C N Q T I M E Q G C C K G F F	344
1201	CGGGCCTGACTGCACGCAGTGTCTGGGGCTCTCCAACCCCTGCTATGGCAAAGGCAA	1260
345	G P D C T Q C P G G F S N P C Y G K G N	364
1261	TTGCAGTGATGGATCCAGGGCAATGGGGCTGCCCTGCTCTGCTTCCCAGACTACAAGGGCAT	1320
365	C S D G I Q G N G A C L C F P D Y K G I	384
1321	CGCCTGCCACATCTGCTCGAACCCAAACAAAGCATGGAGAGCAATGCCAGGAAGACTGCGG	1380
385	A C H I C S N P N K H G E Q C Q E D C G	404
1381	CTGTGTCCATGGTCTCTGCGACAACCGCCCAGGCAGTGGGGGGTGTGCCAGCAGGGCAC	1440
405	C V H G L C D N R P G S G G V C Q Q G T	424
1441	GTGTGCCCTGGCTTCAGTGGCCGGTCTGCAACGAGTCCATGGGGACTGTGGGCCAC	1500
425	C A P G F S G R F C N E S M G D C G P T	444
1501	AGGGCTGGCCAGCACTGCCACCTGCATGCCGCTGTGTAGCCAGGAGGTGTGCCAG	1560
445	G L A Q H C H L H A R C V S Q E G V A R	464
1561	ATGTCGCTGTCTTGATGGCTTGAGGGTGATGGCTCTCCTGCACACCTAGCAACCCCTG	1620
465	C R C L D G F E G D G E S C T P S N P C	484
1621	CTCCCCACCCGGACCGTGGAGGCTGCTCAGAGAAATGCTGAGTGTGTCCCTGGTCCCTGGG	1680
485	S H P D R G G C S E N A E C V P G S L G	504

Figure 1C

1681	CACCCACCACTGCACATGCCACAAAGGCTGGAGTGGGGATGGCCGCGTCTGTGTGGCTAT	1740
505	T H H C T C H K G w s a d a x v c v a I	524
1741	TGACGAGTGTGAGCTGGACGTGAGAGGTGGCTGCCACACCGATGCCCTCTGCAGCTATGT	1800
525	D E C E L D V R G G C H T D A L C S Y V	544
1801	GGGCCCCGGGCAGAGCCGATGCACCTGCAAGCTGGGCTTGCCGGGGATGGCTACCAAGTG	1860
545	G P G Q S R C T C K L G E A G D G Y Q C	564
1861	CAGCCCCATCGACCCCTGCCGGGCAAGGCAATGGCGGCTGCCACGGCCTGGAGCTGGAGGC	1920
565	S P I D P C R A G N G G C H G L E L E A	584
1921	AAATGCCCACTTCTCCATCTTCTACCAATGGCTTAAGAGTGCAGGCTACGCTTCCCTGC	1980
585	N A H F S I F Y Q W L K S A G I T L P A	604
1981	CGACCGCCGAGTCACAGCCCTGGTGCCCTCCGAGGCTGCAGTCGGTCAGCTGAGCCCCGA	2040
605	D R R V T A L V P S E A A V R Q L S P E	624
2041	GGACCGAGCTTCTGGCTGCAGCCAGGACGCTGCCAACCTGGTCAGGGCCATTCT	2100
625	D R A F W L Q P R T L P N L V R A H F L	644
2101	CCAGGGTGCCCTTCGAGGAGGAGCTGGCCGGCTGGTGGGCAGGAAGTGGCCACCC	2160
645	Q G A L F E E E L A R L G G Q E V A T L	664
2161	GAACCCCACACAGCTGGAGATTGCAACATTAGTGGGAGGGCTGGGTGCAGAATGC	2220
665	N P T T R W E I R N I S G R V W V Q N A	684
2221	CAGCGTGGATGTGGCTGACCTCCTGCCACCAACGGTGTCTACACATCCTCAGCCAGGT	2280
685	S V D V A D L L A T N G V L H I L S Q V	704
2281	CTTACTGCCCCCCCGAGGGATGTGCCCGGTGGCAGGGTTGCTGCAGCAGCTGGACTT	2340
705	L L P P R G D V P G G Q G L L Q Q L D L	724
2341	GGTGCCTGCCCTCAGCCTCTCCGGGAATTGCTGCAGCACCATGGTTGGTGCAGAT	2400
725	V P A F S L F R E L L Q H H G L V P Q I	744
2401	TGAGGCTGCCACTGCCACACCATCTTGTGCCACCAACCGCTCCCTGGAGGGCCAGGG	2460
745	E A A T A Y T I F V P T N R S L E A Q G	764
2461	CAACAGCAGTCACCTGGACGCAGACACAGTGCAGGCACCATGTGGTCTGGGGAGGCCCT	2520
765	N S S H L D A D T V R H H V V L G E A L	784

Figure 1D

2521	CTCCATGGAAACCCCTGGGAAGGGTGGACACCGCAACTCCCTCCTGGGCCCTGCCCACTG	2580
785	S M E T L R K G G H R N S L L G P A H W	804
2581	GATCGTCTCTACAACCACAGTGGCCAGCCTGAGGTGAACCATGTGCCACTGGAAGGCC	2640
805	I V F Y N H S G Q P E V N H V P L E G P	824
2641	CATGCTGGAGGCCCTGGCCGCTCGCTGATTGGCTCTGTCGGGGTCCTGACGGTGGCCTC	2700
825	M L E A P G R S L I G L S G V L T V G S	844
2701	AAGTCGCTGCCCTGCATAGCCACGCTGAGGCCCTGCGGGAGAAATGTGTAAACTGCACCA	2760
845	S R C L H S H A E A L R E K C V N C T R	864
2761	GAGATTCCCGCTGCACTCAGGGCTTCCAGCCTGCAGGACACACCCAGGAAGAGCTGTCTA	2820
865	R F R C T Q G F Q L Q D T P R K S C V Y	884
2821	CCGATCTGGCTTCTCCTCTCCGGGCTGCTCTAACATGTGCCAAGAAGATCCAGGT	2880
885	R S G F S F S R G C S Y T C A K K I Q V	904
2881	GCCGGACTGCTGCCCTGGTTCTTGGCACGCTGTGAGCCATGCCAGGGGTCTAGG	2940
905	P D C C P G F F G T L C E P C P G G L G	924
2941	GGGGGTGTGCTCAGGCCATGGCAGTGCCAGGACAGGTTCCCTGGCAGCGGGAGGTGCCA	3000
925	G V C S G H G Q C Q D R F L G S G E C H	944
3001	CTGCCACGAGGGCTTCCATGGAACGCCCTGTGAGGTGTGAGCTGGCCCTACGGGCC	3060
945	C H E G F H G T A C E V C E L G R Y G P	964
3061	CAACTGCACCGGAGTGTGTGACTGTGCCCATGGCTGTGCCAGGAGGGCTGCAAGGG	3120
965	N C T G V C D C A H G L C Q E G L Q G D	984
3121	CGGAAGCTGTGCTGTAACGTGGCTGGCAGGGCTCCGCTGTGACCAAGAAAATCACCAG	3180
985	G S C V C N V G W Q G L R C D Q K I T S	1004
3181	CCCTCAGTGCCCTAGGAAGTGCACGGCCAAATGCCAATGCCACTGCGTGCAGGACTCGGCCGGAGC	3240
1005	P Q C P R K C D P N A N C V Q D S A G A	1024
3241	CTCCACCTGCGCCTGTGCTGGGATACTCCGGAATGGCATCTCTGTTAGAGGTGGA	3300
1025	S T C A C A A G Y S G N G I F C S E V D	1044
3301	CCCCTGCGCCCACGGCCATGGGGCTGCTCCCTCATGCCAATGTACCAAGGTGGCACC	3360
1045	P C A H G H G G C S P H A N C T K V A P	1064

Figure 1E

3361	TGGGCAGCGGACATGCACCTGCCAGGATGGCTACATGGCGACGGGGAGCTGTGCCAGGA	3420
1065	G Q R T C T C Q D G Y M G D G E L C Q E	1084
3421	AATTAACAGCTGTCTCATCCACCACGGGGCTGCCACATTCAACGCCAGTGCATCCCCAC	3480
1085	I N S C L I H H G G C H I H A E C I P T	1104
3481	TGGCCCCAGCAGGTCTCCTGCAGCTGCCGTGAGGGTTACAGCGGGATGGCATCCGGAC	3540
1105	G P Q Q V S C S G R E G Y S G D G I R T	1124
3541	CTGCGAGCTCCTGGACCCCTGCTCTAAGAACAAATGGAGGATGCCAGCCCATAATGCCACCTG	3600
1125	C E L L D P C S K N N G G C S P Y A T C	1144
3601	CAAAAGCACAGGGATGCCAGAGGACATGTACCTGCGACACAGCCCACACCGTGGGGGA	3660
1145	K S T G D G Q R T C T C D T A H T V G D	1164
3661	CGGCCTCACCTGCCGTGCCCGAGTCGGCCTGGAGCTCTGAGGGATAAGCATTGCCTCATT	3720
1165	G L T C R A R V G L E L L R D K H A S F	1184
3721	CTTCAGCCTCCGCCTCTGGAATATAAGGAGCTAAGGGCGATGGGCCTTCACCATCTT	3780
1185	F S L R L L E Y K E L K G D G P F T I F	1204
3781	CGTGCCGCAGCAGATCTAATGAGCAACCTGTCGCAGGATGAGCTGGCCCGATTGTC	3840
1205	V P H A D L M S N L S Q D E L A R I R A	1224
3841	GCATGCCAGCTGGTGTTCGCTACCACGTGGTTGGCTGCGCCGCTGGGAGCGAGGA	3900
1225	H R Q L V F R Y H V V G C R R L R S E D	1244
3901	CCTGCTGGAGCAGGGTACGCCACGGCCCTCTCAGGGCACCCACTGCGCTTCAGCGAGAG	3960
1245	L L E Q G Y A T A L S G H P L R F S E R	1264
3961	GGAGGGCAGCATATACCTCAATGACTTCGCGCGCGTGGTGAGCAGCGACCATGAGGCCGT	4020
1265	E G S I Y L N D F A R V V S S D H E A V	1284
4021	GAACGGCATCCCTGCACCTTCATTGACCGTGTCCCTGCTGCCCGGAGGCGCTGCACGGGA	4080
1285	N G I L H F I D R V L L P P E A L H W E	1304
4081	GCCTGATGATGCTCCCATCCCGAGGAGAAATGTCACCGCCGCCGCCAGGGCTTCGGTTA	4140
1305	P D D A P I P R R N V T A A A Q G F G Y	1324
4141	CAAGATCTTCAGCGGCCCTCTGAAGGTGGCCGGCTCCTGCCCTGCTTCGAGAGGCATC	4200
1325	K I F S G L L K V A G L L P L L R E A S	1344

Figure 1F

4201	CCATAGGCCCTCACAAATGCTGTGGCCCACAGACGCCGCTTTCGAGCTCTGCCCTCCGGA	4260
1345	H R P F T M L W P T D A A F R A L P P D	1364
4261	TCGCCAGGCCTGGCTGTACCATGAGGACCACCGTGACAAGCTAGCAGCCATTCTGCGGGG	4320
1365	R Q A W L Y H E D H R D K L A A I L R G	1384
4321	CCACATGATTGCAATGTCGAGGCCCTGGCATCTGACCTGCCAACCTGGCCACTTCG	4380
1385	H M I R N V E A L A S D L P N L G P L R	1404
4381	AACCATGCATGGGACCCCCATCTCTTCTCCTGCAGCCGAACGCCGGCCCGGTGAGCTCAT	4440
1405	T M H C P I S F S C S R T R P G E L M	1424
4441	GGTGGGTGAGGATGATGCTCGCATTGTGCAGCGGCACCTGCCCTTGAGGGTGGCCTGGC	4500
1425	V G E D D A R I V Q R H L P F E G G L A	1444
4501	CTATGGCATCGACCAGCTGCTGGAGCCACCTGCCCTGGTGCTGCTGTGACCACTTG A	4560
1445	Y G I D Q L L E P P G L G A R C D H F E	1464
4561	GACCCGGCCCTGCGACTGAACACCTGCAGCATTGTGGCTGGAGCCACCTGTCCGA	4620
1465	T R P L R L N T C S I C G L E P P C P E	1484
4621	GGGGTCACAGGAGCAGGGCAGCCCTGAGGCCCTGGCGCTCTACCGAAGTTCTGGAC	4680
1485	G S Q E Q G S P E A C W R F Y P K F W T	1504
4681	GTCCCCCTCCGCTGCACTCTTGGGATTACGCAGCGTCTGGTCCACCCAGCCTTGGG G	4740
1505	S P P L H S L G L R S V W V H P S L W G	1524
4741	TAGGCCCAAGGCCCTGGCAGGGCTGCCACCGAATTGTGTCAACCACCTGGAAAGCC	4800
1525	R P Q G L G R G C H R N C V T T T W K P	1544
4801	CAGCTGCTGCCCTGGTCACTATGGCAGTGAGTGCCAAAGCTGCCCTGGCGCCAGCAG	4860
1545	S C C P G H Y G S E C Q A C P G G P S S	1564
4861	CCCTTGAGTGACCGTGGCGTGTGCATGGACGGCATGAGTGGCAGTGGCAGTGTCTGTG	4920
1565	P C S D R G V C M D G M S G S G Q C L C	1584
4921	CCGTTCAAGGTTTGCTGGACAGCCGTGTGAACCTCTGTGCTCTGGTGCCTTGGGCCCA	4980
1585	R S G E A G T A C E L C A P G A F G P H	1604
4981	TTGTCAAGGCCCTGCCGCTGCACTGTGCATGGCCGCTGTGATGAGGGCCTGGGGCTCTGG	5040
1605	C Q A C R C T V H G R C D E G L G G S G	1624

Figure 1G

5041	CTCCTGCTCTGTGATGAAGGCTGGACTGGGCCACGCTGTGAGGTGCAACTGGAGCTGCA	5100
1625	S Q F Q D E G W T G P R Q E V Q L E L Q	1644
5101	GCCTGTGTACCCCCACCCGTGCACCCGAGGCTGTGTGCCGTGCAGGCAACAGCTGTGA	5160
1645	P V C T P P C A P E A V C R A G N S Q E	1664
5161	GTGCAGCCTGGCTATGAAGGGATGGCCGTGTGTACAGTGGCAGACCTGTGCCAGGA	5220
1665	C S L G Y E G D G R V Q T V A D L C Q D	1684
5221	CGGGCATGGTGGCTGCAGTGAGCACGCCAACTGTAGCCAGGTAGGAACAAATGGTCACTTG	5280
1685	G H G G C S E H A N C S Q V G T M V T C	1704
5281	TACCTGCCTGCCGACTACGAGGGTGTGGCTGGAGCTGCCGGGCCGCAACCCCTGCAC	5340
1705	T C L P D Y E G D G W S C R A R N P C T	1724
5341	AGATGGCCACCGCGGGGCTGCAGCGAGCACGCCAACTGCTTGAGCACCCGCTGAACAC	5400
1725	D G H R G G C S E H A N C L S T G L N T	1744
5401	ACGGCGCTGTGAGTGCACGCAGGCTACGTAGCGATGGACTGCAGTGTCTGGAGGAGTC	5460
1745	R R C E C H A G Y V G D G L Q C L E E S	1764
5461	GGAAACCACTGTGGACCGCTGCTGGGCCAGCCACCGCCCTGCCACTCAGATGCCATGTG	5520
1765	E P P V D R C L G Q P P P C H S D A M C	1784
5521	CACTGACCTGCACTTCCAGGAGAAACGGCTGGCTTTCCACCTCCAGGCCACCAGCGG	5580
1785	T D L H F Q E K R A G V F H L Q A T S G	1804

5581	CCCTTATGGTCTGAACCTTTCGGAGGCTGAGCCGGCATGCGAAGCACAGGGAGCCGTCC	5640
1805	<u>P Y G L N F S E A E A A C E A Q G A V L</u>	1824

5641	TGCTTCATTCCCTCAGCTCTGTGTGCCAGCAGCTGGCTTCCACCTGTGCCTCATGGG	5700
1825	<u>A S F P Q L S A A Q Q L G F H L C L M G</u>	1844

5701	CTGGCTGGCCAATGGCTCCACTGCCACCCCTGTGGTTTCCCTGTGGCGGACTGTGGCAA	5760
1845	<u>W L A N G S T A H P V V F P V A D C G N</u>	1864

5761	TGGTCGGGTGGCATAGTCAGCCTGGTGCCCCAAGAACCTCTCAGAACGCTGGGATGC	5820
1865	<u>G R V G I V S L G A R K N L S E R W D A</u>	1884

Figure 1H

5821	CTACTGCTCCGTGTGCAAGATGTGGCCTGCCGATGCCGAAATGGCTTCGTGGGTGACGG	5880
1885	<u>Y C F R V Q D V A C B C R N G E V G D G</u>	1904
5881	GATCAGCACGTGCAATGGGAAGCTGCTGGATGTGCTGGCTGCCACTGCCAACTTCTCCAC	5940
1905	I S T C N G K L L D V L A A T A N F S T	1924
5941	CTTCTATGGGATGCTATTGGGCTATGCCAATGCCACCCAGCGGGGTCTCGACTTCTCGGA	6000
1925	F Y G M L L G Y A N A T Q R G L D F L D	1944
6001	CTTCCTGGATGATGAGCTACGTATAAGACACTCTTCGTCCCTGTCAATGAAGGCTTTGT	6060
1945	F L D D E L T Y K T L F V P V N E G F V	1964
6061	GGACAACATGACGCTGAGTGGCCCAAACCTGGAGCTGCATGCCCTCAACGCCACCCCT	6120
1965	D N M T L S G P K L E L H A S N A T L L	1984
6121	AAGTGCCAACGCCAGCCAGGGGAAGTTGCTTCCGGCCCACTCAGGCCTCAGCCTCATCAT	6180
1985	S A N A S Q G K L L P A H S G L S L I I	2004
6181	CAGTGACGCCAGGCCCTGACAACAGTTCCCTGGGCCCTGTGGCCCAAGGGACAGTTGTGGT	6240
2005	S D A G P D N S S W A P V A P G T V V V	2024
6241	TAGCCGTATCATGGTGGGACATCATGGCCTTCATGGCATCATCCATGCTCTGGCCAG	6300
2025	S R I I V W D I M A F N G I I H A L A S	2044
6301	CCCCCTCCTGGCACCCCCACAGCCCCAGGCAGTGCTGGCGCTGAAGCCCCACCTGTGGC	6360
2045	P L L A P P Q P Q A V L A X E A P P V A	2064
6361	GGCAGGCCGTGGGGCTGTGCTTGCGCTGGAGCACTGCTTGCTTGGCTGGCCGGAGCTCT	6420
2065	A G V G A V L A A G A L L L G L V A G A L	2084
6421	CTACCTCCGTGCCGAGGCAAGCCCATGGCTTGGCTTCTCTGCCCTCCAGGCCGAAGA	6480
2085	Y L R A R G K P M G F G F S A F Q A E D	2104
6481	TGATGCTGATGACGANITCTCACCGTGGCAAGAAGGGACCAACCCACNTGGTNTNTGT	6540
2105	D A D D X F S P W Q E G T N P T L V X V	2124
6541	CCCCAACCTGTCTTGGCAGCGACACCTTTGTGAACCCCTCGATGACTCACTGCTGGA	6600
2125	P N P V F G S D T F C E P F D D S L L E	2144
6601	GGAGGACTTCCCTGACACCCAGAGGATCCTCACAGTCAGTGACGAGGCTGGGCTGAAA	6660
2145	E D F P D T Q R I L T V K *	2158

6661 GCAGAAGCATGCACAGGGAGGAGACCAN^TTTATTGCTTGTCTGGGTGGATGGGGCAGGA 6720

6721 GGGNCTGAGGGCCTGTCCCAGACAATANNNGTNCCTCGAG 6761

Figure 2A

1	GAGCACGCCAACTGTAGCCAGGTAGGAACAATGGTCACTTGTACCTGCCCTGCCCGACTAC	60
1	M V T C T C L P D Y	10
61	GAGGGTGTGGCTGGAGCTGCCGGGCCGCAACCCCTGCACAGATGGCCACCGCGGGGGC	120
11	E G D G W S C R A R N P C T D G H R G G	30
121	TGCAGCGAGCACGCCAACTGCTTGAGCACCCGCCCTGAACACACAGCGCTGTGAGTGCCAC	180
31	C S E H A N C L S T G L N T R R C E C H	50
181	GCAGGCTACGTAGGCGATGGACTGCACTGGAGGAGTCGGAACCACCTGTGGACCGC	240
51	A G Y V G D G L Q C L E E S E P P V D R	70
241	TGCTTGCCAGCCACCGCCCTGCCACTCAGATGCCATGTGCACTGACCTGCACCTCCAG	300
71	C L G Q P P P C H S D A M C T D L H F Q	90
301	GAGAAACGGCTGGCGTTTccACCTCCAGGCCACCAGCGGCCCTTATGGTCTGAACCTT	360
91	<u>E K R A G V F H L Q A T S G P Y G L N F</u>	110
361	*****	420
111	<u>T C G G A G G C T G A G G C G G C A T G C G A A G C A C A G G G A G C C G T C C T T G C T T C A T T C C C T C A G C T C</u>	130
421	*****	480
131	<u>T C T G C T G C C C A G C A G C T G G G C T T C C A C C T G T G C C T C A T G G G C T G G C T G G C C A A T G G C T C C</u>	150
481	*****	540
151	<u>A C T G C C C A C C T G T G G T T T C C C T G T G G C G A C T G T G G C A A T G G T C G G G T G G G C A T A G T C</u>	170
541	*****	600
171	<u>T A H P V V F P V A D C G N G R V G I V</u>	190
601	AGCCTGGGTGCCCGCAAGAACCTCTCAGAACGCTGGGATGCCACTGCTTCCGTGTGCAA	660
191	<u>S L G A R K N L S E R W D A Y C F R V Q</u>	210
661	GATGTGGCTGCCGATGCCGAAATGGCTCGTGGGTGACGGGATCAGCACCGTCAATGG	720
211	<u>D V A C R Q R N G F V G D G I S T C N G</u>	230
721	AAGCTGCTGGATGTGCTGGCTGCCACTGCCAACTTCTCCACCTCTATGGGATGCTATTG	780
231	<u>K L L D V L A A T A N F S T F Y G M L L</u>	250
781	GGCTATGCCAATGCCACCCAGCGGGGTCTGACTTCCTGGACTTCCTGGATGATGAGCTC	840
	ACGTATAAGACACTCTCGTCCCTGTCAATGAAGGCTTGTGGACAACATGACGCTGAGT	

251 T Y K T L F V P V N E G F V D N M T L S 270

Figure 2B

841	GGCCCAAACCTGGAGCTGCATGCCCTCAACGCCACCCCTCTAAGTGCCAAACGCCAGCCAG	900
271	G P N L E L H A S N A T L L S A N A S Q	290
901	GGGAAGTTGCTTCCGGCCCCTCAGGCCCTCAGCCCTCATCATCAGTGACGCAGGCCCTGAC	960
291	G K L L P A H S G L S L I I S D A G P D	310
961	AACAGTTCTGGGCCCTGTGGCCCCAGGGACAGTTGTGGTAGCCGTATCATTGTGTGG	1020
311	N S S W A P V A P G T V V V S R I I V W	330
1021	GACATCATGCCCTCAATGGCATCATCCATGCTCTGGCCAGCCCCCTCCCTGGCACCCCCA	1080
331	D I M A F N G I I H A L A S P L L A P P	350
1081	CAGCCCCAGGCAGTGCTGGCGNTGAAGCCCCACCTGTGGCGGCAGGCGTGGGGCTGTG	1140
351	Q P Q A V L A X E A P P V A A G V G A V	370
1141	CTTGCCGCTGGAGCACTGCTTGGCTTCTCTGGCTACCTCCGTGCCCGAGGC	1200
371	L A A G A L L G L V A G A L Y L R A R G	390
1201	AAGCCCATGGCTTGGCTCTCTGGCTTCCAGGCGGAAGATGATGCTGATGACGANTTC	1260
391	K P M G F G F S A F Q A E D D A D D D X F	410
1261	TCACCGTGGCAAGAAGGGACCAACCCACNITGGTNTNTGTCCCCAACCTGTCTTGGC	1320
411	S P W Q E G T N P T L V X V P N P V F G	430
1321	AGCGACACCTTTGTGAACCCCTCGATGACTCACTGCTGGAGGAGGACTTCCCTGACACC	1380
431	S D T F C E P F D D S L L E E D F P D T	450
1381	CAGAGGATCCTCACAGTCAAGTGACGAGGCTGGGCTGAAAGCAGAACATGCACAGGGA	1440
451	Q R I L T V K *	458
1441	GGAGACCANTTTATTGCTTGTCTGGTGGATGGGCAGGAGGGNCTGAGGGCTGTCCC	1500
1501	AGACAAATANNNGTNCCCTCGAG	1522

Figure 3A

1	GCCCCACGCGTCCGACCGGGACAGCTCGCGCCCCNAGAGCTAGCCGTNGAGGAGCTG	60
61	CCTGGGGACGTTTGCCCTGGGGCCCCAGCCTGGCCCGGGTCACCCCTGGCATGAGGAGATG	120
1	M	1
121	GGCCTGTTGCTCCTGGTCCCATTGCTCCCTGCTGCCCGGCTCCTACGGACTGCCCTCTAC	180
2	G L L L L V P L L L P G S Y G L P F Y	21
181	TACGGCTTCTACTACTCCAACAGCGCCAACGACCAGAACCTAGGCAACGGTCATGGCAA	240
22	Y G F Y Y S N S A N D Q N L G N G H G K	41
241	GACCTACNTAATGGAGTGAAGCTGGTGGAGACACCCGAGGAGACCCCTGTTCACCTAC	300
42	D L X N G V K L V V E T P E E T L F T Y	61
301	CAAGGGGCCAGTGTGATCCTGCCCTGCCGCTACCGCTACGAGCCGGCCCTGGTCTCCCCG	360
62	Q G A S V I L P C R Y R Y E P A L V S P	81
361	CGGCGTGTGCGTGTCAAATGGTGGAAAGCTGTCGGAGAACGGGGCCCCAGAGAAGGACGTG	420
82	R R V R V K W W K L S E N G A P E K D V	101
421	CTGGTGGCCATCGGGCTGAGGCACCGCTCCTTGGGACTACCAAGGCCGCGTGCACCTG	480
102	<u>L V A I G L R H R S F G D Y Q G R V H L</u>	121
481	CGGCAGGACAAAGAGCATGACGTCTCGNTGGAGATCCAGGNTCTGGCTGGAGGACTAT	540
122	<u>R Q D K E H D V S X E I Q X L R L E D Y</u>	141
541	GGCGTTACCGCTGTGAGGTCACTNGACGGCTGGAGGATGAAAGCGGTCTGGTGGAGCTG	600
142	<u>G R Y R C E V X D G L E D E S G L V E L</u>	161
601	GAGCTGCGGGGTGTGGCTTCCCTACCAAGTCCCCAACGGCGCTACCAAGTTCAACTTC	660
162	<u>E L R G V V F P Y Q S P N G R Y Q F N F</u>	181

661	CACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGTGGCTGGCTCCCTTGAGCAGCTC	720
182	H E G Q Q V C A E Q A A V V A S F E Q L	201

721	TTCCGGGCCTGGAGGAGGGCCTGGACTGGTCAACGCCGGCTGGCTGCAGGATGCCACG	780
202	F R A W E E G <u>L D W C N A G W L Q D A T</u>	221

781	GTGCAGTACCCCATCATGTTGCCCGCAGCCCTGCGTGGCCGGACCTGGCACCTGGC	840
222	<u>V Q Y P I M L P R Q P C G G P D L A P G</u>	241

Figure 3B

841 GTGCGAAGCTACGGCCCCGCCACCGCCGCTGCACCGCTATGATGTATTCTGCCTCGCT 900
242 V R S Y G P R H R R L H R Y D V F C F A 261

901 ACTGCCCTCARGGGGGGGGTGTACTACCTGGANCACCCCTGAGAANCTGACNCTGACANAA 960
262 T A L X G R V Y Y L X H P E X L T L T X 281

961 GCAAGGGAAGCCTGCCAAGAAAAAT 985
282 A R E A C Q E K 289

Figure 4A

1	GGAATCACATGCACAGTTGGATTTyTGCAAACAGGACAACGGGGCTGTGCAAAGGTG	60
61	GCCAGATGCTCCCAGAAGGGCACGAAGGTCTCCTGCAGCTGCCAGAAGGGATACAAAGGG	120
121	GACGGGCACAGCTGCACAGAGATAGACCCCTGTGCAGACGGCTTAACGGAGGGTGTAC	180
181	GAGCACGCCACCTGTAAGATGACAGGCCGGCAAGCACAAGTGTGAGTGTAAAAGTCAC	240
1	M T G P G K H K C E C K S H	14
241	TATGTCGGAGATGGGCTGAAGTGTGAGCCGGAGCAGCTGCCATTGACCGCTGCTTACAG	300
15	Y V G D G L N C E P E Q L P I D R C L Q	34
301	GACAATGGGCAGTGCCATGCAGACGCCAAATGTGTCGACCTCCACPTCCAGGGATAACACT	360
35	D N G Q C H A D A K C V D L H F Q D T T	54
361	GTTGGGGTGTCCATCTACGCTCCCCACTGGGCCAGTATAAGCTGACCTTTGACAAAGCC	420
55	V G V F H L R S P L G Q Y K L T F D K A	74
421	AGAGAGGCCCTGTGCCAACGAAAGCTGCGACCATGGCAACCTACAACCAGCTCTCCTATNNC	480
75	R E A C A N E A A T M A T Y N Q L S Y X	94
481	CAGAAGGCCAACGATACCACCTGTGCTCAGCAGGCTGGCTGGAGACCGGGCGGGTTGCCAAC	540
95	Q K A K Y H L C S A G W L E T G R V A Y	114
541	CCCACAGCCTTCGCTCCCAGAACTGTGGCTCTGGTGTGGTTGGGATAGTGGACTATGGA	600
115	P T A F A S <u>Q N C G S G V V G I V D Y G</u>	134
601	CCTAGACCCAACAAGAGTGAAATGTGGGATGTCTCTGCTATCGGATGAAAGATGTGAAC	660
135	<u>P R P N K S E M W D V F C Y R M K D V N</u>	154
661	TGCACCTNCAAGGTGGCTATGTGGGAGATGGCTTCTCATaCAGTGGAACCTGCTGCAG	720
155	<u>C T X K V G Y V G D G F S Y S G N L L Q</u>	174
721	GTCCTGATGTCCTTCCCTCACTCACAAACTTCTGACGGAAAGTGGCTGGCTATTCCaaC	780
175	<u>V L M S F P S L T N F L T E V L A Y S N</u>	194
781	AGcTCAGcTCGAGGCCGtGCATTCTAGAACACCTGACTGACCTGTCCATCCGcGGCACC	840
195	<u>S S A R G R A F L E H L T D L S I R G T</u>	214

Figure 4B

841	CTCTtTGTNccACAGAACAGTGGgCTGGGGGAGAATGAGACCTTGTCTGGGcGGGACATC	900
215	<u>L</u> F V P Q N S G L G E N E T L S G R D I	234
901	GAGCACCACCTGCCAATGTCAGcATGTTTtTCTACAAATGACCTtTgtCAATGGCACCACC	960
235	E H H L A N V S M F F Y N D L V N G T T	254
961	CTGCAAACGGAGGcTGGGAAGCAAgCTGCTCATCACTGacAGaCAGGACCCACTCCAccCCG	1020
255	L Q T R L G S K L L I T D R Q D P L H P	274
1021	AcGGAGACCAGGTgTGTGATGGAAGAgACtCTGgAGtGGGACATCTgTGcCTCCAAAT	1080
275	T E T R C V D G R D T L E W D I C A S N	294
1081	GGgatCACAcATGTCATTCCAGGyCTTTAAaAGCACCCCCCTgCCCCCGtGAcCttGNCC	1140
295	G I T H V I S R X L K A P P A P V T L X	314
1141	CACACTGgNTtGGGAgNAGGGATCTCTINTGNCATCATCCTGGTGAATGGGGCTGTTGCC	1200
315	H T G L G X G I F X X I I L V T G A V A	334
1201	TTGGCTGCTTACTCCTACTTCGGATAAACCGGAAACAAATCGGCTTCCANCATTTGA	1259
335	L A A Y S Y F R I N R K T I G F X H F	353

Figure 5A

10 20 30
1 M M D Q G C R E I L T T A G P F T V L V P S V S S F S S R T WF-HABP (FL).filed.aa
1 T M ----- Human TSG-6 (gi|339994)
40 50 60
31 M N A S L A Q O Q L C R O H I I A G O H I L E D T R T O O T R WF-HABP (FL).filed.aa
7 ----- Human TSG-6 (gi|339994)
70 80 90
61 R W W T L A G Q E I T V T F N Q F T K Y S Y K Y K D Q P Q Q WF-HABP (FL).filed.aa
7 ----- Human TSG-6 (gi|339994)
100 110 120
91 T F N I Y K A N N I A A N G V F H V V T G L R W Q A P S G T WF-HABP (FL).filed.aa
7 ----- Human TSG-6 (gi|339994)
130 140 150
121 P G D P K R T I G Q I L A S T E A F S R F E T I L E N C G L WF-HABP (FL).filed.aa
7 R R T K D K T A S R T E ----- Human TSG-6 (gi|339994)
160 170 180
151 P S I L D G P G P F T V F A P S N E A V D S L R D G R L I Y WF-HABP (FL).filed.aa
43 ----- Human TSG-6 (gi|339994)
190 200 210
181 L F T A G L S K L Q E L V R Y H I Y N H G Q L T V E K L I S WF-HABP (FL).filed.aa
43 ----- S Human TSG-6 (gi|339994)
220 230 240
211 K G R I L T M A N Q V L A V N I S E E G R I L L G P E G V P WF-HABP (FL).filed.aa
46 K G ----- Human TSG-6 (gi|339994)
250 260 270
241 L Q R V D V M A A N G V I H M L D G I L L P P T I L P I L P WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)
280 290 300
271 K H C S E E Q H K I V A G S C V D C Q A L N T S T C P P N S WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)
310 320 330
301 V K L D I F P K E C V Y I H D P T G L N V L K K G C A S Y C WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)

Figure 5B

340 350 360
331 NOTIMEOGCCKGFFGPDCTOCPGGFSNPCY WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)

370 380 390
361 GKGNCSDGIQGNGACLCFPDYKGIACHICS WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)

400 410 420
391 NPNKHGEQCOEDCGCVHGLCDNRPGSGGVC WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)

430 440 450
421 QQGTCAPGFSGRFCNE SMGDCGPTGLAQHC WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)

460 470 480
451 HLHARCVSQEGVARCRCLDGFEGDGFSCTP WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)

490 500 510
481 SNPCSHPDRGGCSENAECSVPGSLGTHHCTC WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)

520 530 540
511 HKGWSGDGRVCVAIDECELDVRGGCHTDAL WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)

550 560 570
541 CSYVGPGQSRCCTCKLGFAGDGYQCSPTIDPC WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)

580 590 600
571 RAGNGGCHGLELEANAHFSIFYQOWLKSAGI WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)

610 620 630
601 TLPADRRVTALVPSEAAVRQLSPEDRAFWL WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)

640 650 660
631 QPRTLPNLVRAHFLQGALFEEELARLGGOE WF-HABP (FL).filed.aa
52 ----- Human TSG-6 (gi|339994)

Figure 5C

670 680 690
661 VATLNPTTRWEIRNISGRVWVQNAASVVDVAD WF-HABP (FL).filed.aa
52 - - - - - TRKEAGRVTKONPK - - - Human TSG-6 (gi|339994)

700 710 720
691 LLATNGVLHILSQVLLPPRGDVPGGQGLLO WF-HABP (FL).filed.aa
94 - - - - - Human TSG-6 (gi|339994)

730 740 750
721 QLDLVPAFSLFRELLQHHGLVPQIEAATAY WF-HABP (FL).filed.aa
94 - - - - - Human TSG-6 (gi|339994)

760 770 780
751 TIFVPTNRSLEAQGNSSHLDADTVRHUVVL WF-HABP (FL).filed.aa
94 - - - - - Human TSG-6 (gi|339994)

790 800 810
781 GEALSMETLRKGGHHRNSLLGPAHWIVFYNH WF-HABP (FL).filed.aa
94 - - - - - Human TSG-6 (gi|339994)

820 830 840
811 SGOPEVNHVPLEGPMLEAPGRSLIGLSGVL WF-HABP (FL).filed.aa
94 - - - - - Human TSG-6 (gi|339994)

850 860 870
841 TVGSSRCLHSHAEALREKCVNCTRFRCTQ WF-HABP (FL).filed.aa
94 - - - - - Human TSG-6 (gi|339994)

880 890 900
871 GFOLODTPRKSCVYRSGFSFSGRCSYTCAK WF-HABP (FL).filed.aa
94 - - - - - Human TSG-6 (gi|339994)

910 920 930
901 KIQVPDCCPGFFGTLCEPCPGGLGGVCSGH WF-HABP (FL).filed.aa
94 - - - - - Human TSG-6 (gi|339994)

940 950 960
931 GOCQDRFLGSGECHCHEGFHGTACEVCELG WF-HABP (FL).filed.aa
94 - - - - - Human TSG-6 (gi|339994)

970 980 990
961 RYGPNCCTGVCDCAHGLCQEGLQGDGSVCVN WF-HABP (FL).filed.aa
94 - - - - - Human TSG-6 (gi|339994)

Figure 5D

1000 1010 1020
 991 V G W Q G L R C D Q K I T S P Q C P R K C D P N A N C V Q D WF-HABP (FL) .filed.aa
 94 - - - - - Human TSG-6 (gi|339994)

1030 1040 1050
 1021 S A G A S T C A C A A G Y S G N G I F C S E V D P C A H G H WF-HABP (FL) .filed.aa
 94 - - - - - Human TSG-6 (gi|339994)

1060 1070 1080
 1051 G G C S P H A N C T K V A P G Q R T C T C Q D G Y M G D G E WF-HABP (FL) .filed.aa
 94 - - - - - Human TSG-6 (gi|339994)

1090 1100 1110
 1081 L C Q E I N S C L I H H G G C H I H A E C I P T G P Q Q V S WF-HABP (FL) .filed.aa
 94 - - - - - Human TSG-6 (gi|339994)

1120 1130 1140
 1111 C S C R E G Y S G D G I R T C E L L D P C S K N N G G C S P WF-HABP (FL) .filed.aa
 94 - - - - - Human TSG-6 (gi|339994)

1150 1160 1170
 1121 Y A T C K S T G D G Q R T C T C D T A H T V G D G L T C R A WF-HABP (FL) .filed.aa
 94 - - - - - Human TSG-6 (gi|339994)

1180 1190 1200
 1171 R V G L E L L R D K H A S F F S L R L L E Y K E L K G D G P WF-HABP (FL) .filed.aa
 94 - - - - - Human TSG-6 (gi|339994)

1210 1220 1230
 1201 F T I F V P H A D L M S N L S Q D E L A R I R A H R Q L V F WF-HABP (FL) .filed.aa
 94 - - - - - Human TSG-6 (gi|339994)

1240 1250 1260
 1231 R Y H V V G C R R L R S E D L L E Q G Y A T A L S G H P L R WF-HABP (FL) .filed.aa
 109 - - - - - Human TSG-6 (gi|339994)

1270 1280 1290
 1261 F S E R E G S I Y L N D F A R V V S S D H E A V N G I L H F WF-HABP (FL) .filed.aa
 109 - - - - - Human TSG-6 (gi|339994)

1300 1310 1320
 1291 I D R V L L P P E A L H W E P D D A P I P R R N V T A A A Q WF-HABP (FL) .filed.aa
 109 - - - - - Human TSG-6 (gi|339994)

Figure 5E

1330 1340 1350

1321 G F G Y K I F S G L L K V A G I L P L L R E A S H R P F T M WF-HABP (FL).filed.aa
130 - - - - - Human TSG-6 (gi|339994)

1360 1370 1380

1351 L W P T D A A F R A L P P D R Q A W L Y H E D H R D K L A A WF-HABP (FL).filed.aa
130 - - - - - Human TSG-6 (gi|339994)

1390 1400 1410

1381 I L R G H M I R N V E A L A S D L P N L G P L R T M H G T P WF-HABP (FL).filed.aa
151 - - - - - Human TSG-6 (gi|339994)

1420 1430 1440

1411 I S F S C S R T R P G E L M V G E D D A R I V Q R H L P F E WF-HABP (FL).filed.aa
151 - - - - - Human TSG-6 (gi|339994)

1450 1460 1470

1441 G G L A Y G I D O L L E P P G L G A R C D H F E T R P L R L WF-HABP (FL).filed.aa
151 - - - - - Human TSG-6 (gi|339994)

1480 1490 1500

1471 N T C S I C G L E P P C P E G S Q E Q G S P E A C W R F Y P WF-HABP (FL).filed.aa
151 - - - - - Human TSG-6 (gi|339994)

1510 1520 1530

1501 K F W T S P P L H S L G L R S V W V H P S L W G R P Q G L G WF-HABP (FL).filed.aa
151 - - - - - Human TSG-6 (gi|339994)

1540 1550 1560

1531 R G C H R N C V T T T W K P S C C P G H Y G S E C Q A C P G WF-HABP (FL).filed.aa
151 - - - - - Human TSG-6 (gi|339994)

1570 1580 1590

1561 G P S S P C S D R G V C M D G M S G S G Q C L C R S G F A G WF-HABP (FL).filed.aa
151 - - - - - Human TSG-6 (gi|339994)

1600 1610 1620

1591 T A C E L C A P G A F G P H C O A C R C T V H G R C D E G L WF-HABP (FL).filed.aa
151 - - - - - Human TSG-6 (gi|339994)

1630 1640 1650

1621 G G S G S C F C D E G W T G P R C E V Q L E L Q P V C T P P WF-HABP (FL).filed.aa
166 - - - - - Human TSG-6 (gi|339994)

Figure 5F

1651	CAPEAVCRAGNSCECSLGYEGDGRVCTVAD	WF-HABP (FL).filed.aa
166	-----	Human TSG-6 (gi 339994)
<hr/>		
1681	LCQDGHHGGCSEHANCSEQVGTMVTCCLPDY	WF-HABP (FL).filed.aa
166	-----	Human TSG-6 (gi 339994)
<hr/>		
1711	EGDGWSSCRARNPCTDGHHRGGCSEHANCLST	WF-HABP (FL).filed.aa
166	-----	Human TSG-6 (gi 339994)
<hr/>		
1741	GLNTRRCCECHAGYVGDGLOQLEESEPPVDR	WF-HABP (FL).filed.aa
166	-----	Human TSG-6 (gi 339994)
<hr/>		
1771	CLGQPPPCHSDAMCTDLHFQEKRAGVFHLQ	WF-HABP (FL).filed.aa
166	-----	Human TSG-6 (gi 339994)
<hr/>		
1801	ATSGPYGLNFSEAEAACEAQGAVLASFPOL	WF-HABP (FL).filed.aa
175	-----	Human TSG-6 (gi 339994)
<hr/>		
1831	SAAQOLGFHLCLMGWLNGSTAHPVVFPVA	WF-HABP (FL).filed.aa
175	-----	Human TSG-6 (gi 339994)
<hr/>		
1861	DCGNGRVGIIVSLGARKNLSERWDAYCFRVQ	WF-HABP (FL).filed.aa
175	-----	Human TSG-6 (gi 339994)
<hr/>		
1891	DVACRCRNGFVGDGISTCNGKLLDVLAATA	WF-HABP (FL).filed.aa
175	-----	Human TSG-6 (gi 339994)
<hr/>		
1921	NFSTFYGMLLGYNATQRGFLDFLDDEL	WF-HABP (FL).filed.aa
175	-----	Human TSG-6 (gi 339994)
<hr/>		
1951	TYKTLFVPVNNEGFDVNMTLSGPNLELHASN	WF-HABP (FL).filed.aa
175	-----	Human TSG-6 (gi 339994)

Figure 5G

1990 2000 2010

1981 175 AT LLSA N A S O G K L L P A H S G L S L I I S D A G P D WF-HABP (FL).filed.aa
Human TSG-6 (gi|339994)

2020 2030 2040

2011 175 N S S W A P V A P G T V V V S R I I V W D I M A F N G I I H WF-HABP (FL).filed.aa
Human TSG-6 (gi|339994)

2050 2060 2070

2041 175 A L A S P L L A P P Q P Q A V L A X E A P P V A A G V G A V WF-HABP (FL).filed.aa
Human TSG-6 (gi|339994)

2080 2090 2100

2071 178 L A A G A L L G L V A G A L Y L R A R G K P M G F G F S A F WF-HABP (FL).filed.aa
Human TSG-6 (gi|339994)

2110 2120 2130

2101 178 Q A E D D A D D D X F S P W Q E G T N P T L V X V P N P V F G WF-HABP (FL).filed.aa
Human TSG-6 (gi|339994)

2140 2150 2160

2131 187 S D T F C E P F D D S L L E E D F P D T Q R I L T V K WF-HABP (FL).filed.aa
Human TSG-6 (gi|339994)

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Figure 6

WF-HABP AA SEQUENCE*
Human TSG-6 (gi|339994)

10 20 30

1 M V T C T C L P D Y E G D G W S C R A R N P C T D G H R G G
1 T M - - - P R T E D E T A S R T E G K G

40 50 60

31 C S E H A H C L S T G L H T P R R C E C H A G Y V G D G L O C
32 - - - - - T R R - - - - -

70 80 90

61 L E E S E P P V D R C L G O P P P C H S D A M C T D L H F Q
61

100 110 120

91 E K R A G V F H L O A T S G P Y G L M F S E A E A A C E A Q
91

130 140 150

121 G A V L A S F P Q L S A A Q Q L G F H L C L M G W L A N G S
61

160 170 180

151 T A H P V V F P V A D C G N G R V G I V S L G A R K N L S E
61 E A G R V T - - - - - E Q N P K

190 200 210

181 R W D A Y C F R V O D V A C R C R N G F V G D G I S T C N G
94 R

220 230 240

211 K L L D V L A A T A N F S T F Y G M L L G Y A N A T Q R G L
97

250 260 270

241 D F L D F L P D E L T Y K T L F V P V N E G F V D N H T L S
97

280 290 300

271 G P N L E L H A S M A T L L S A N A S Q G K L L P A H S C L
97

310 320 330

301 S L I T S D A G P D N S S W A P V A P G T V V V S R I I V W
97

340 350 360

331 D I M A F E N G I I H A L A S P L L A P P O P Q A V L A X E A
97 I E R

370 380 390

361 E P V A A G V G A V L A A G A L L G L V A G A L Y L R A R G
106 Q P - - - - - K R T

400 410 420

391 K E H M G F G F S A F Q A E D D A D D E X F S P W O E G T N P T
121 K A - - - - - T H Q K - - - - - R P K

430 440 450

421 L V X V P M P V F G S D T F C E P F D D S L L E E D F E D T
148 L K C - - - - - N I G Q K

460

451 Q R I T L T V K
172 R R I F - - . E D I X

WF-HABP AA SEQUENCE*
Human TSG-6 (gi|339994)

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Figure 7

OE-HABP ORF Sequence
Cartilage Link (gi|212260).aa

10 20 30

1 M G L L L L V P L L L P G S Y G L P F Y Y G F Y Y S H S N
1 M T S L L F - - L V L I S V C W A E E - - - - - H P

40 50 60

31 N D Q N L G N G H G K D L X - - N G V K L V V E T P E E T L
20 E N S S L E H E R I I H I Q E E N G P R L L V V A E Q A K I

70 80 90

59 F T Y Q G A S V I L P C R Y R Y E P A L V S - - - P R R V R
50 F S Q R G G N V T L P C K F Y H E H T S T A G S G T H K I R

100 110 120

86 V K W W K L S E N G A P E K D V I V A I G L R H R S F G D Y
80 V K W T K I L T S D Y L K E V D V F V A M G H H R K S Y C K Y

130 140 150

116 Q G R V H L R O D K E H D V S X E I O X L E F L E D Y G R Y R
110 Q G R V F L R E S S E N D A S L T I T N I M L E D Y G R Y K

160 170 180

146 C E V X D G L E D E S G L V E L E L R G V V F P Y O S P N G
140 C E V I E G L E D D T A V V A L I N L E G V V F P Y S P R L G

190 200 210

176 R Y Q F N F H E G Q Q V C A E Q A A V V A S F E Q L F R A W
170 R Y N L N F H E A Q Q A C L D Q D S I T A S F D O L Y E A W

220 230 240

206 F E G L D W C N A G W L Q D A T V Q Y P I M L P R Q P C G G
200 F S G L D W C N A G W L S D G S V O Y P I T K P R E P C G G

250 260 270

236 P D L A P G V R S Y G E F H R R I H R Y D V F C F A T A L X
230 K N T V P G V R N Y G F W D K E R S R Y D V F C F T S N F N

280 290 300

266 G R V Y Y L X H P E X L T F L T X A R E A C Q - - - - -
260 G R F Y Y L I H P T K L T Y D E A V Q A C L K D G A Q I A K

310 320 330

288 - - - - -
290 V G Q T F A A W K L L G Y D R C D A G W L A D G S V R Y P I

340 350 360

288 - - - - -
320 S R P R K R C S P N E A A V R E V G F P D K K H K L Y G V Y

288 - - - - - E K
350 C F R A Y N .

OE-HABP ORF Sequence
Cartilage Link (gi|212260).aa

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Figure 8

1	10	20	30	EM-HABP AA SEQUENCE*
1	M T G P G K H K C E C K S H Y V G D G L C E P E O L F I D			TSG-6 (GI 2062475).AA
1	M V - - - - -		- V L	
31	40	50	60	EM-HABP AA SEQUENCE*
5	R C L O D U G O C H A D A K C V D L - - - - -			TSG-6 (GI 2062475).AA
5	L C L - - - - - C V L L W E F A R G W G F R K H G			
49	70	80	90	EM-HABP AA SEQUENCE*
24	H F Q E T - - - T V G V F H L R S P L G O Y K L T E D K			TSG-6 (GI 2062475).AA
24	I F H N S I W L E Q A A G V Y H R E A R A G R Y K L T Y A E			
74	100	110	120	EM-HABP AA SEQUENCE*
54	A R E A C A H E A A T M A T Y N Q L S Y X Q K A K Y H L C S			TSG-6 (GI 2062475).AA
54	A K A V C E F E G G R L A T Y K O L E A A R K I G F H V C A			
104	130	140	150	EM-HABP AA SEQUENCE*
84	A G W I L E T G R V A Y P T A F A S O N C G S G V V G I V D Y			TSG-6 (GI 2062475).AA
84	A G W M A K G R V G Y P I V K P C P N C G F G K T G I I D Y			
134	160	170	180	EM-HABP AA SEQUENCE*
114	G P R E N K S E M W D V F C Y R H K D W N C T X - - - - - K			TSG-6 (GI 2062475).AA
114	G I R L M R S E R W D A Y C Y N P H A K E C G G V F T D P K			
159	190	200	210	EM-HABP AA SEQUENCE*
144	V G Y V G D G F S - - Y S G H L L - - - - - Q V			TSG-6 (GI 2062475).AA
144	R I F E K S P E G P F H E Y D D N N Q V C Y W H I E L R Y C O R I			
176	220	230	240	EM-HABP AA SEQUENCE*
174	L M S P F P E - - - - - I T N F L T E V I L A Y S N S S			TSG-6 (GI 2062475).AA
174	H L S F L D F D L E H D P G C L A D Y V E I Y D S Y D D V R			
197	250	260	270	EM-HABP AA SEQUENCE*
204	A R G F A F L E H L T D I S I R G T L F V P Q - - N S G L C			TSG-6 (GI 2062475).AA
204	G - - - - - F V U G R Y C G D E L P			
225	280	290	300	EM-HABP AA SEQUENCE*
216	E N E T L S G R D I E H H L A N V S M F F Y N D L V N G T T			TSG-6 (GI 2062475).AA
216	E D I T I S T G N V M T L E F - - - - - I S D A S V			
255	310	320	330	EM-HABP AA SEQUENCE*
236	L Q T R L G S K L L I T D R O D P L H P T E T R C V D G R D			TSG-6 (GI 2062475).AA
236	T A G G F Q I K Y V T V D - - - - P A S K S S Q A K N			
285	340	350	360	EM-HABP AA SEQUENCE*
259	T L E W D I C A S N G I T H V I S R X L K A P P A P V T L X			TSG-6 (GI 2062475).AA
259	T - - - - - S T T G N K K F I L P - - - - -			
315	370	380	390	EM-HABP AA SEQUENCE*
270	H T G L G X G I F X X I I L V T G A V A L A B A Y S Y F R I N			TSG-6 (GI 2062475).AA
270	- - - - - C R F S H L .			
345	395	405	415	EM-HABP AA SEQUENCE*
276	R K T I G F X H F			TSG-6 (GI 2062475).AA

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Figure 9

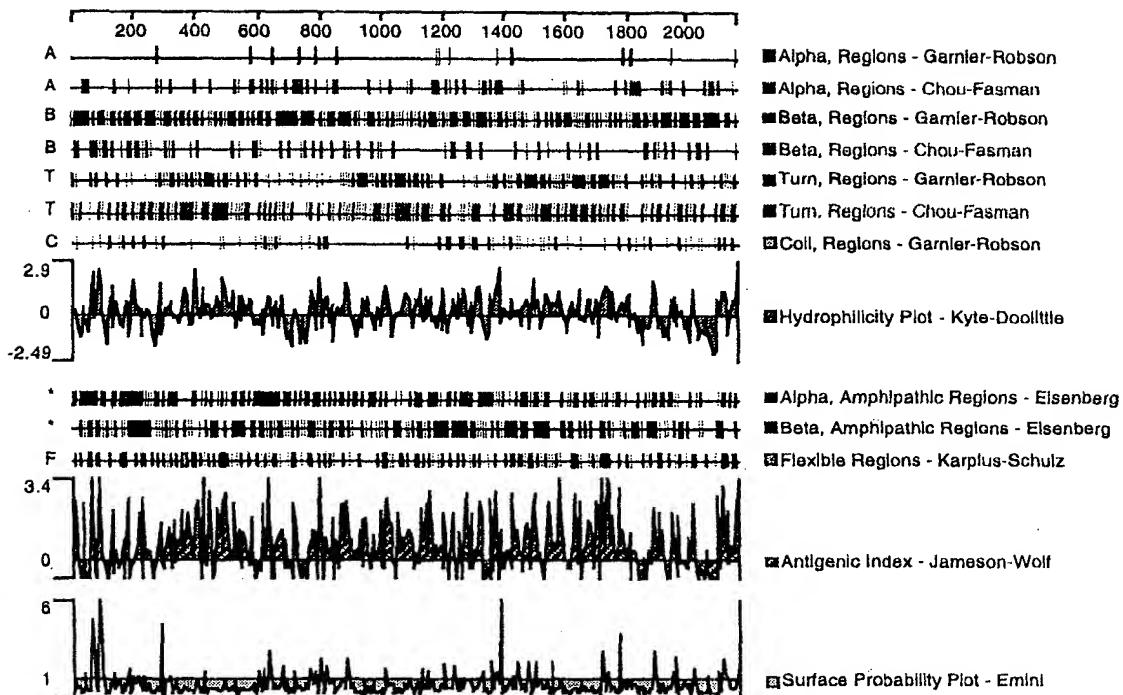


Figure 10

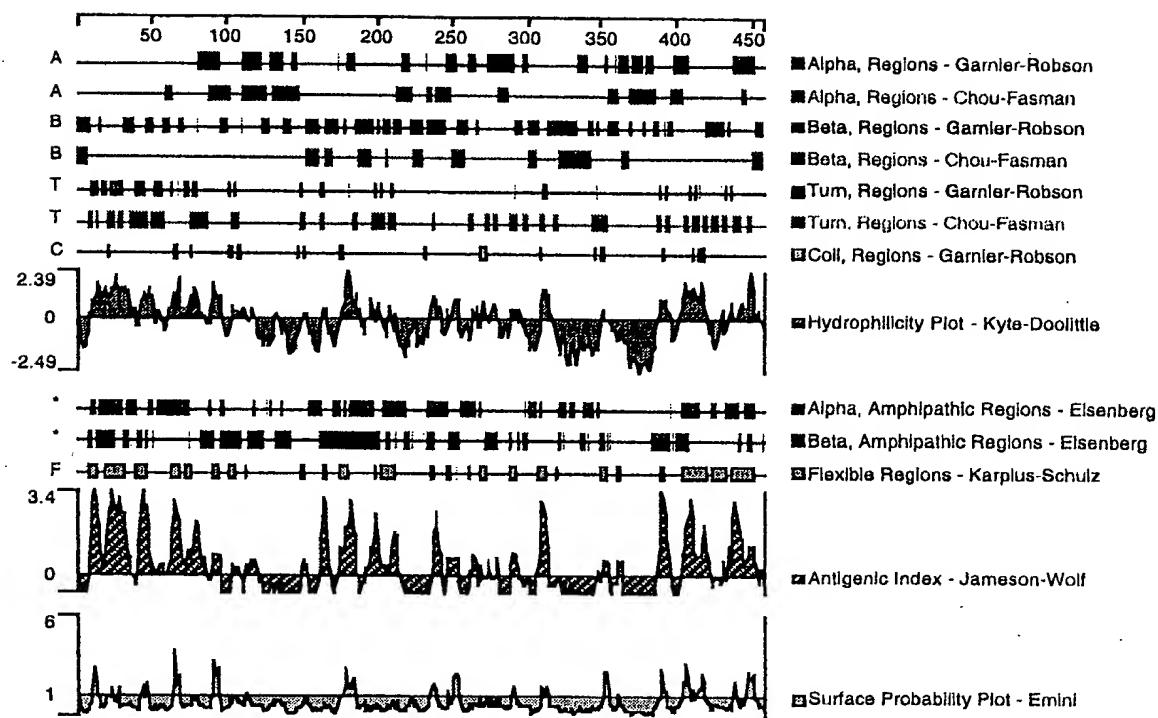


Figure 11

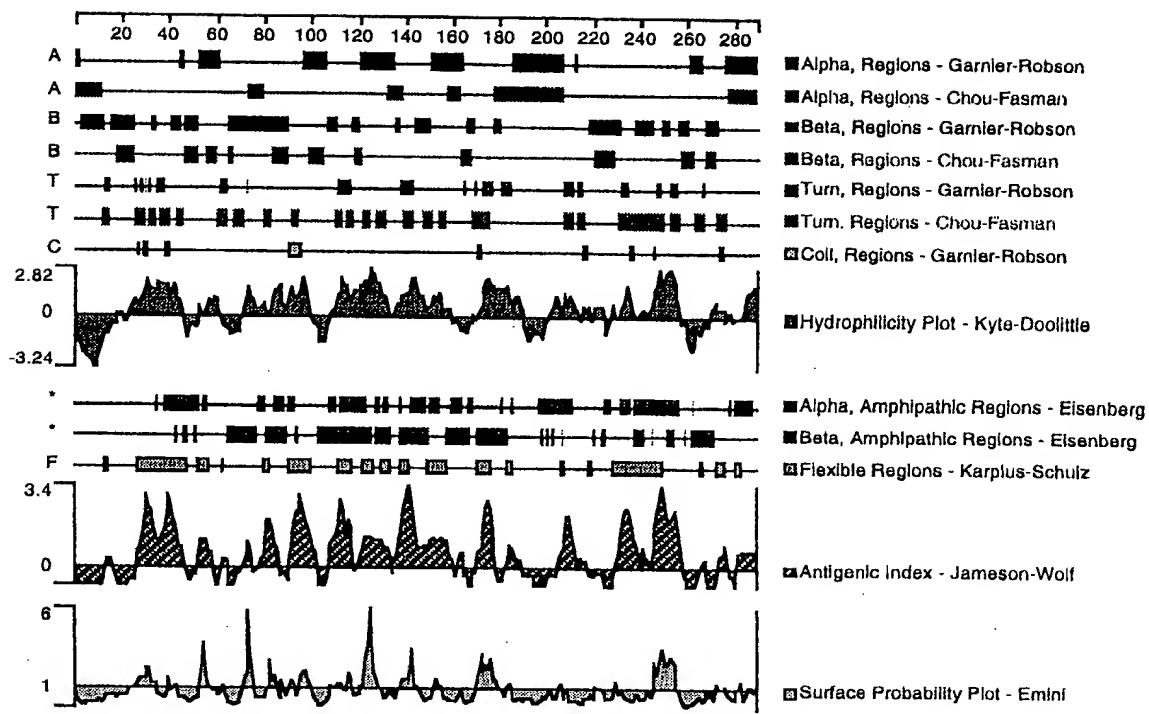


Figure 12

